

REMARKS/ARGUMENTS

Status of the Claims

Upon entry of the present response, claims 27-35 and 37-38 are pending. Claims 27-35 are withdrawn as directed to a non-elected invention. Claims 37-38 are under examination. No amendments are made to the claims.

Request for Rejoinder

Pursuant to M.P.E.P. § 821.04, Applicants respectfully request rejoinder of method claims 27-35. In accordance with M.P.E.P. § 821.04, Applicants amended claim 27 in a previously submitted response to correspond to the scope of claim 37.

Rejection under 35 U.S.C. § 103(a)

The Examiner has maintained the rejection claims 37 and 38 under 35 U.S.C. § 103(a) as allegedly rendered obvious over U.S. Patent No. 5,858,752 ("Seed") in view of Sasaki, *et al.*, *J Biol Chem* (1994)269:14730-14737 ("Sasaki"). This rejection is respectfully traversed because Seed is not prior art, and Sasaki does not disclose or suggest any murine Fuc-TVII enzyme.

In the Advisory Action mailed on July 24, 2007, the Examiner acknowledged that the Exhibit B accompanying the Rule 131 Declaration of Kevin Gersten submitted on March 20, 2007 shows actual reduction to practice. However, the Examiner has requested additional evidence to show that page 104 identified in Exhibit B and discussed in the Rule 131 Declaration of Kevin Gersten contains the Fuc-TVII gene. In response, Applicants provide a second Rule 131 Declaration from Dr. John Lowe, co-inventor with and supervisor to Dr. Kevin Gersten and Dr. Shunji Natsuka. Dr. Lowe submits with his Declaration copies from orders of primers used to sequence the Fuc-TVII gene in page 104.¹ As the Examiner can see, the primers were ordered by co-inventor Dr. Gersten, and the primers are interchangeably referenced

¹ The copies of the orders of the FucT-VII/page 104 primers, with dates redacted, are attached as Exhibit C. A list of the primers is attached as Exhibit D.

as phage 104 or FucT-VII. The primers include 624B and 625B, discussed in the previous response and Rule 131 Declaration of Kevin Gersten. Dr. Lowe also provides with his Declaration the full sequence of the mouse FucT-VII gene, sequenced from phage 104 and annotated to show the annealing positions of the primers used to sequence the Fuc-TVII gene.² As the Examiner can see, in the annotated FucT-VII gene sequence, the primers as listed in Exhibit D are in bold; forward primers are labeled above the primer sequence and reverse primers are labeled below the primer sequence. Moreover, when the sequence from phage 104 shown in Exhibit E is subject to a BLAST alignment against the mouse genome database, the only transcript that is retrieved is for mouse fucosyltransferase VII (GenBank accession number NM_013524).³ A BLAST alignment also confirms that the sequence of phage 104 shares effectively 100% sequence identity with SEQ ID NO:1 of the present application. Finally, Dr. Lowe provides a notebook page from co-inventor Dr. Shunji Natsuka.⁴ The page from Dr. Natsuka's notebook records a Southern blot of the mouse FucT-VII gene ("mFT7"). This notebook page is another example of the interchangeable reference to the mouse FucT-VII gene and phage 104. That is, it is clear that scientists in Dr. Lowe's laboratory, including co-inventors Drs. Lowe, Gersten and Natsuka, recognized that phage 104 contained the sequence of mouse FucT-VII. The objective sequences of the primers and the full length sequence from phage 104 are consistent with the conclusion that phage 104 contained mouse FucT-VII.

In view of the evidence provided with Dr. Lowe's Declaration and the present response, it is clear that phage 104 referenced in Exhibit B contained the sequence of the mouse FucT-VII gene. The Examiner acknowledges that Exhibit B clearly demonstrates the reduction to practice of the amplification of a sequence encoding the stem and catalytic domains of mouse Fuc-TVII from a mouse nucleic acid sequence captured in phage 104.

Therefore, in accordance with M.P.E.P. § 715.02, Applicants have demonstrated possession of the basic inventive concept of what is claimed before the effective filing date of the Seed reference. In view of the further evidence presented with the present response, Exhibit B

² The annotated sequence of the mouse FucT-VII gene is provided as Exhibit E.

³ BLAST sequence alignments and report for NM_013524 are provided as Exhibit G.

demonstrates using the primers as taught on page 47 of the specification and as claimed to amplify and clone a sequence encoding the stem and catalytic domains of mouse Fuc-TVII. Therefore, the Rule 131 Declarations of Drs. Gersten and Lowe are sufficient to overcome the rejection based on the Seed reference because Seed is not prior art.

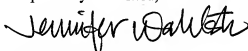
Therefore, for the reasons set forth in the previous responses and herein, Applicants respectfully maintain that the present invention is not obvious over Seed in view of Sasaki because Seed is not prior art. Accordingly, the Examiner is respectfully requested to withdraw this rejection.

CONCLUSION

In view of the foregoing, Applicants believe all claims now pending in this Application are in condition for allowance and an action to that end is respectfully requested.

If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at 415-576-0200.

Respectfully submitted,



Jennifer L. Wahlsten
Reg. No. 46,226

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Fax: 415-576-0300
Attachments
JLW:jlw
61182944 v1

⁴ The page from Dr. Natsuka's notebook, with dates redacted, is provided as Exhibit F.

BIOMEDICAL RESEARCH CORE FACILITIES
DNA SYNTHESIS CORE 2556 MSRB II 764-1451

Synthesis Request Sheet

☒ Applied Biosystems G 497810

CLIENT USE ONLY:

Sequence # 3242 B

Column

☒ Applied Biosystems G 497852

RR

Date Synthesized

D.G.

Order's Date:
Requestor: Gersten
P.I. Name: LOWE
Billing Dept.: HHMI
Phone Number: 7-4756
Account Number: 921099

Sequence Length: 36
Synthesis Scale: 0.2 umole
Trityl Group: ___On ___X___ Off
Thio-Chemistry: ___Yes ___X___ No

BA

SEQUENCE. 5' -> 3', IN TRIPLET (* PLEASE START WITH A TRIPLET *)

GCG CCT CGA GCA AAC AGG AAG GAC AGC AGG CTC TGG

User Comments:

ELC-VII genomic pcr bp 9-34 5' pcr exon 1

Comments to Core Facility:

- 184 Synthesis Setup Listing -

(Version 1.02)

Column 1

Run ID :
Cycle : Cvc01 user
End Proc: End CE DMT = Off)
Sequence: 3242B

Total bases = 36

A= 10, G= 13, C= 10, T= 3, 5= 0, 6= 0, 7= 0, 8= 0
(mixed bases= 0)

HW: 11142.2

5'> GCG CCT CGA GCA AAC AGG AAG GAC AGC AGG CTC TGG <3'

Synthesis Request Sheet

D. G.

```
Sequence Length: 20
Synthesis Scale: 0.2 umole
Trityl Group:    ___On   _X_  Off
Thio-Chemistry:  ___Yes  _X_  No
```

$$A_{200} = .240$$

42nd 1958

BIOMEDICAL RESEARCH CORE FACILITIES
DNA SYNTHESIS CORE 2562 MSRB II 764-1461

Synthesis Request Sheet

FACILITY USE ONLY:

Sequence #

☒ Applied Biosystems C 483928

9392A

Column

☒ Applied Biosystems C 483082

Date Synthesized

12/6

Today's Date:

Requestor:

Gersten

P.I. Name:

LOWE

Billing Dept.:

HHMI

Phone Number:

7-4756

Account Number: 030131

Sequence Length: 20

Synthesis Scale: 0.2 umole

Trityl Group: ___On ___X___ Off

Thio-Chemistry: ___Yes ___X___ No

SEQUENCE, 5'→ 3', IN TRIPLETS (* PLEASE START WITH A TRIPLET *)

GCT AGA TAG TTT CTG ATG GC

OD₂₆₀ 1.00 = .141

User Comments:

Fuct7-1

25/1ml

Comments to Core Facility:

- 394 Synthesis Setup Listing -

(Version 2.00)

Column 2

Run ID :

Cycle : Cyc01 user

End Proc: End CE (DMT = Off)

Sequence: 9392A

Total bases = 20

A= 4, G= 6, C= 3, T= 7, 5= 0, 6= 0, 7= 0, 8= 0
(mixed bases= 0)

MW: 6158.0

5'→ GCT AGA TAG TTT CTG ATG GC <3'

BIOMEDICAL RESEARCH CORE FACILITIES
DNA SYNTHESIS CORE 2562 MSRB II 764-1461

Synthesis Request Sheet

FACILITY USE ONLY:	Sequence #	1042 B
	Column	Applied Biosystems C 436432
	Date Synthesized	⑤
Today's Date:	Sequence Length:	20
Requestor: Gersten	Synthesis Scale:	0.2 umole
P.I. Name: LOWE	Trityl Group:	___On ___X Off
Billing Dept.: HHMI	Thio-Chemistry:	___Yes ___X No
Phone Number: 7-4754		
Account Number: 921099		

SEQUENCE, 5'→ 3', IN TRIPLETS (* PLEASE START WITH A TRIPLET *)

GTA TGG GTG CCA TCA GAA AC

User Comments:

104 sal-eco from 986 towards 5' UT

Comments to Core Facility:

- 394 Synthesis Setup Listing - (Version 1.01)

Column 4

Run ID :
Cycle : Cyc01 user
End Proc: End CE (DMT = Off)
Sequence: 1042B

Total bases = 20

A= 6, G= 6, C= 4, T= 4, 5= 0, 6= 0, 7= 0, 8= 0
(mixed bases= 0)

MW: 6654.0

5' GTA TGG GTG CCA TCA GAA AC <3'

$A_{260} = .217$

46/954

Synthesis Request Sheet

FACILITY USE ONLY:

Sequence #

8660A

Column

489821

Date Synthesized

DM (E)

Today's Date:

Requestor: Gersten

P.I. Name: LOWE

Billing Dept.: HHMI

Phone Number: 7-4756

Account Number: 030131

Sequence Length: 20

Synthesis Scale: 0.2 umole

Trityl Group: ___On ___X Off

Thio-Chemistry: ___Yes ___X No

SEQUENCE, 5'→ 3', IN TRIPLETS (* PLEASE START WITH A TRIPLET *)

CAG GGC ACT TCT GAG GTG CC

User Comments:

Fuc-TVII bp424 sequencing primer towards 3' end

Comments to Core Facility:

1/100 = .905

25/1ml

- 394 Synthesis Setup Listing - (Version 1.01)

Column 3

Run ID :

Cycle : Cyc01 user

End Proc: End CE (DMT = Off)

Sequence: 8660A

Total bases = 20

A= 3, G= 7, C= 6, T= 4, 5= 0, 6= 0, 7= 0, 8= 0
(mixed bases= 0)

NW: 6573.0

5'→ CAG GGC ACT TCT GAG GTG CC <3'

BIOMEDICAL RESEARCH CORE FACILITIES
DNA SYNTHESIS CORE 2562 MSRB II 764-1461

Synthesis Request Sheet

Applied Biosystems G 495751

FACILITY USE ONLY:

Sequence #

9393A

Column

Applied Biosystems G 472563

Date Synthesized

D.G.

Today's Date:

Requestor: Gersten

P.I. Name: LOWE

Billing Dept.: HHMI

Phone Number: 7-4756

Account Number: 030131

Sequence Length: 20

Synthesis Scale: 0.2 umole

Trityl Group: ___On ___X___ Off

Thio-Chemistry: ___Yes ___X___ No

SEQUENCE, 5'→ 3', IN TRIPLETS (* PLEASE START WITH A TRIPLET *)

AAC AGC AGC CTT GTC ACG TG

User Comments:

Fuct7-2

OD 260 / 1,00 = .156

26/1ml

Comments to Core Facility:

- 394 Synthesis Setup Listing -

(Version 2.00)

Column 3

Run ID :

Cycle : Cyc01 user

End Proc: End CE

Sequence: 9393A (DMT = Off)

Total bases = 20

A= 5, G= 5, C= 6, T= 4, 5= 0, 6= 0, 7= 0, 8= 0
(mixed bases= 0)

MW: 6098.0

5'> AAC AGC AGC CTT GTC ACG TG <3'

BIOMEDICAL RESEARCH CORE FACILITIES
DNA SYNTHESIS CORE 2562 MSRB II 764-1461

Synthesis Request Sheet

FACILITY USE ONLY:

Sequence #

986 B

Column

~~421275~~ C 421275

Date Synthesized

(B)

Today's Date:

Sequence Length: 20

Requestor: Gersten

Synthesis Scale: 0.2 umole

P.I. Name: LOWE

Trityl Group: ___On ___X___ Off

Billing Dept.: HHMI

Thio-Chemistry: ___Yes ___X___ No

Phone Number: 7-4778

Account Number: 921099

SEQUENCE, 5'→ 3', IN TRIPLETS (* PLEASE START WITH A TRIPLET *)

CAG CCA TAG TCT CAC GTG AC

User Comments:

104 sal-eco from 887 primer towards sal site (5' UT)

Comments to Core Facility: Synthesis Setup Listing -

(Version 1.01)

Column 3

Run ID :

Cycle : Cyc01 user

End Proc: End CE (DMT = Off)

Sequence: 986B

Total bases = 20

A= 5, G= 4, C= 7, T= 4, 5= 0, 6= 0, 7= 0, 8= 0
(mixed bases= 0)

MW: 6536.0

5' CAG CCA TAG TCT CAC GTG AC <3'

. 272

Jul 1963

Synthesis Request Sheet

FACILITY USE ONLY:

Sequence #

672 B

Column

Applied Systems C 410014

Date Synthesized

D.G

Today's Date:

Sequence Length: 20

Requestor: Gersten

Synthesis Scale: 0.2 umole

P.I. Name: LOWE

Trityl Group: On X Off

Billing Dept.: HHMI

Thio-Chemistry: Yes X No

Phone Number: 7-4778

Downloaded from <http://ajph.org/> on November 10, 2015

Account Number: 921099

SEQUENCE, 5'→ 3', IN TRIPLETS (* PLEASE START WITH A TRIPLET *)

CGA AGT GTA GGA AGT GAT CC

User Comments:

104 from 15/52 large (Xho-Kpn) towards 3' end

Comments to Core Facility:

- 394 Synthesis Setup Listing -

(Version 1.01)

Column 2

Run ID :

Cycle : Cyc01 user

End Proc: End CE (DMT = Off)

Sequence: 672B

Total bases = 20

A= 6, G= 7, C= 3, T= 4, 5= 0, 6= 0, 7= 0, 8= 0
(mixed bases= 0)

MW: 6693.0

✓ 5' > CGA AGT GTA GGA AGT GAT CC <3'

$$\therefore \frac{1}{260} = .304$$

33 2 1967

Synthesis Request Sheet

35 ul / 965

Report for Synthetic Oligonucleotide

Date:

Investigator: LOWE
Individual User: Gersten

System Id: 8993

Product Information

Length: 20

Oligonucleotide Sequence:
AGG AAG CTT ABC TAA AAG CT

Comments:

104 phage from t7 primer towards 3' end of gene (5' ut towards gene)

Trityl Group: Off

Synthesis Scale: 0.2 Micromole Scale

Date Received:

Date Synthesised:

Number of Day(s) in the System: 2

If you have any problems, contact the Biopolymers Facility
Your assigned System Id number is 8993
Thank you for using the HHMI Biopolymer Facility.

Use 104Sec PCR ODA

$A_{260} = .264$

38 μ l / 962

BIOMEDICAL RESEARCH CORE FACILITIES
DNA SYNTHESIS CORE 2562 MSRB II 734-1461

Synthesis Request Sheet

FACILITY USE ONLY: Sequence # 571 B
Column **Applied Biosystems C** 410554
Date Synthesized **D.G.**
Today's Date: Requestor: Gersten Sequence Length: 20
P.I. Name: LOWE Synthesis Scale: 0.2 umole
Billing Dept.: HHMI Triton Group: ☐ On ☒ Off
Phone Number: 7-4778 Thio-Chemistry: ☐ Yes ☒ No
Account Number: 921099

SEQUENCE, 5' -> 3', IN TRIPLETS (* PLEASE START WITH A TRIFLET *)

GCA AAG CTA TAG CTT GTA GC

User Comments:

104 from 15/52 (EcoRI) towards 5' end

Comments to Core Facility:

- 394 Synthesis Setup Listing - (Version 1.01)

Column 1

Run ID :
Cycle : Cvc01 user
End Proc: End CE (DMT = Off)
Sequence: 671B

Total bases = 20

A= 6, G= 5, C= 4, T= 5, 5= 0, 6= 0, 7= 0, 8= 0
(mixed bases= 0)

MM: 6629.0

✓ 5' GCA AAG CTA TAG CTT GTA GC <3'

$A_{490} = .319$

31st / 969

BIOMEDICAL RESEARCH CORE FACILITIES
DNA SYNTHESIS CORE 2562 MSRB II 764-1461

Synthesis Request Sheet

FACILITY USE ONLY: Sequence # 3511 B
Column ~~0.2 umol~~ G 404333
Date Synthesized SAS (BA)

Date Submitted: Requestor: Kelly
Phone Number: 74756
Account Number: 921099
P.I. Name: LOWE
Billing Dept.: HHMI
Sequence Length: 20
Synthesis Scale: 0.2 umole
Trityl Group: No
HPLC Purify: No
Thio-Chemistry: No

Center Membership: None
Center/Project Related Research: No

SEQUENCE, 5'→ 3', IN TRIPLETS (* PLEASE START WITH A TRIPLET *)

AGC CTG GAC CTG AGG CTG GG

User Comments:
FT7-1

Comments to Core Facility:

- 394 Synthesis Setup Listing - (Version 2.00)

Column 2

Run ID :
Cycle : Cvc01 user
End Proc: End CE (DMT = Off)
Sequence: 3511B

Total bases = 20

A= 3, G= 9, C= 5, T= 3, 5= 0, 6= 0, 7= 0, 8= 0
(mixed bases= 0)

MW: 6191.0

5'> AGC CTG GAC CTG AGG CTG GG <3'

OD₂₆₀ 1/100 .102

40/ml

BIOMEDICAL RESEARCH CORE FACILITIES
DNA SYNTHESIS CORE 2562 MSRB II 764-1461

Synthesis Request Sheet

FACILITY USE ONLY: Sequence # 946 B
Column ~~4~~ **G** 439403
Date Synthesized D.C.

Today's Date: Requestor: Gersten Sequence Length: 20
P.I. Name: LOWE Synthesis Scale: 0.2 umole
Billing Dept.: HHMI Trityl Group: ___On ___X___ Off
Phone Number: 7-4778 Thio-Chemistry: ___Yes ___X___ No
Account Number: 921099

SEQUENCE, 5' -> 3', IN TRIPLETS (* PLEASE START WITH A TRIPLET *)

TCC TTC CCT TTC CAG ACT GG

User Comments:

104 sac sequencing from 910 towards cat exon

Comments to Core Facility:

- 394 Synthesis Setup Listing - (Version 1.01)

Column 4

Run ID :
Cycle : Cyc01 user
End Proc: End CE (DMT = Off)
Sequence: 946B

Total bases = 20

A= 2, G= 3, C= 8, T= 7, S= 0, 6= 0, 7= 0, 8= 0
(mixed bases= 0)


MW: 6419.0

✓ 5' TCC TTC CCT TTC CAG ACT GG 3'

$A_{260} = .204$

49/957

Synthesis Request Sheet

FACILITY USE ONLY: Sequence # 715 B
Column  C 406550
Date Synthesized -- D.G. --

Today's Date: Requestor: Gersten Sequence Length: 20
P.I. Name: LOWE Synthesis Scale: 0.2 umole
Billing Dept.: HMI Trityl Group: ___ On ☒ Off
Phone Number: 7-4778 Thio-Chemistry: ___ Yes ☒ No
Account Number: 921099

SEQUENCE, 5'→ 3', IN TRIPLETS (* PLEASE START WITH A TRIPLET *)

GGG AAG GAG TCT GTG TGT CC

User Comments:
104 pcr of t cell large frag from sp6 seq

Comments to Core Facility:

COLUMN Z SET-UP
VERSION 2.01

USER_NAME:
CYCLES USED: SSCEAF36- 1
ENDING METHOD: Trityl OFF, Auto
ENDING PROCEDURE: DEPCRE03
SEQUENCE NAME: 715B
SEQUENCE LENGTH: 20
DATE:
TIME:
COMMENT:

✓ 5'- GGG AAG GAG TCT GTG TGT CC -3'

$A_{260} = .304$

33ul / 967

BIOMEDICAL RESEARCH CORE FACILITIES
DNA SYNTHESIS CORE 2562 MSRB II 764-1461

Synthesis Request Sheet

FACILITY USE ONLY:

Sequence # 2931 B

Column

~~Applied Biosystems~~ **G** 479590

Date Synthesized

Chris Batty

Today's Date:

Requestor: Gersten

P.I. Name: LOWE

Billing Dept.: HHMI

Phone Number: 7-4756

Account Number: 921099

Sequence Length: 20

Synthesis Scale: 0.2 umole

Trityl Group: ___ On X Off

Thio-Chemistry: ___ Yes X No

SEQUENCE, 5'→ 3', IN TRIPLETS (* PLEASE START WITH A TRIPLET *)

ACC TTG GGC TGA ACC TAC AG

User Comments:

sequence primer from 946 towards exon 1 S.D. (FT-VII)

Comments to Core Facility:

- 394 Synthesis Setup Listing -

(Version 1.01)

Column 3

Run ID :

Cycle : Cyc01 user

End Proc: End CE (DMT = Off)

Sequence: 2931B

Total bases = 20


A= 5, G= 5, C= 6, T= 4, S= 0, 6= 0, 7= 0, 8= 0
(mixed bases= 0)

MW: 6575.0

5'→ ACC TTG GGC TGA ACC TAC AG <3'

BIOMEDICAL RESEARCH CORE FACILITIES
DNA SYNTHESIS CORE 2562 MSRB II 764-1461

Synthesis Request Sheet

FACILITY USE ONLY: Sequence # 2932 B
Column  460602
Date Synthesized -- Class Bony
Today's Date: Requestor: Gersten Sequence Length: 20
P.I. Name: LOWE Synthesis Scale: 0.2 umole
Billing Dept.: HHMI Trityl Group: ___On ___X___ Off
Phone Number: 7-4756 Thio-Chemistry: ___Yes ___X___ No
Account Number: 921099

SEQUENCE, 5' -> 3', IN TRIPLETS (* PLEASE START WITH A TRIPLET *)

CCT TGA ACT GTA GGT TCA GC

User Comments:

sequence primer proximal to exon 1 S.D towards 5' UT (FT-VII)

Comments to Core Facility:

- 394 Synthesis Setup Listing - (Version 1.01)

Column 2

Run ID :
Cycle : Cyc01 user
End Proc: End CE (DMT = Off)
Sequence: 2932B

Total bases = 20

A= 4, G= 5, C= 5, T= 6, 5= 0, 6= 0, 7= 0, 8= 0
(mixed bases= 0)

MW: 6563.0

5'> CCT TGA ACT GTA GGT TCA GC <3'

BIOMEDICAL RESEARCH CORE FACILITIES
DNA SYNTHESIS CORE 2562 MSRB II 764-1461

Synthesis Request Sheet

FACILITY USE ONLY:

Sequence #

8661A

Column

484064
C

Date Synthesized

CH 18

Today's Date:

Requestor: Gersten

P.I. Name: LOWE

Billing Dept.: HHMI

Phone Number: 7-4756

Account Number: 030131

Sequence Length: 20

Synthesis Scale: 0.2 umole

Trityl Group: ___ On ___ X ___ Off

Thio-Chemistry: ___ Yes ___ X ___ No

SEQUENCE, 5'→ 3', IN TRIPLETS (* PLEASE START WITH A TRIPLET *)

TTT TCT AGA GGT GGC AGA AC

User Comments:

fuc-tvii sequencing primer towards 3' end (bp 1333)

Comments to Core Facility:

1/100 = .443

22.57 / ml

- 394 Synthesis Setup Listing -

(Version 1.01)

Column 3

Run ID :

Cycle : Cyc01 user

End Proc: End CE (DMT = Off)

Sequence: 8661A

Total bases = 20

A= 5, G= 6, C= 3, T= 6, 5= 0, 6= 0, 7= 0, 8= 0
(mixed bases= 0)

MW: 6642.0

5'> TTT TCT AGA GGT GGC AGA AC <3'

Synthesis Request Sheet

FACILITY USE ONLY:

Sequence #

911 B

Column

 C 426226

Date Synthesized

D.C.

Today's Date:

Requestor:

Gersten

P.I. Name:

LOWE

Billing Dept.:

HHMI

Phone Number:

7-4778

Account Number:

921099

Sequence Length:

20

Synthesis Scale:

0.2 umole

Trityl Group:

___On ___X___ Off

Thio-Chemistry:

___Yes ___X___ No

SEQUENCE, 5'→ 3', IN TRIPLETS (* PLEASE START WITH A TRIPLET *)

GGA CCT GTG CTC CCA GAT CC

User Comments:

104 sequencing from sac 9076 primer towards 5' exon

Comments to Core Facility:

- 394 Synthesis Setup Listing -

(Version 1.01)

Column 2

Run ID :

Cycle : Cyc01 user

End Proc: End CE

(DMT = )

Sequence: 911B

Total bases = 20

A= 3, G= 5, C= 8, T= 4, 5= 0, 6= 0, 7= 0, 8= 0

(mixed bases= 0)

MW: 6495.0

✓5' GGA CCT GTG CTC CCA GAT CC <3'

A₁₆₀₂ .215

47 μl / 953

Report for Synthetic Oligonucleotide

Date:

Investigator: LOWE

System Id: 9077

Individual User: Gersten

Product Information

Length: 20

Oligonucleotide Sequence:

AAG GGA TCA CTT CTG CTC AG

Comments:

104phage from 8952 towards 5' end of gene

Trityl Group: Off

Synthesis Scale: 0.2 Micromole Scale

Date Received:

Date Synthesized:

Number of Day(s) in the System: 4

If you have any problems, contact the Biopolymers Facility

Your assigned System Id number is 9077

Thank you for using the HHMI Biopolymer Facility.

$$A_{260} = .219$$

46 μ l / 954

Report for Synthetic Oligonucleotide

Date:

Investigator: LOWE
Individual User: Gersten

System Id: 9076

Product Information

Length: 20

Oligonucleotide Sequence:
TGC TT(CAST) CCT TCA GGA AAA GG

Comments:
104phage from B952 towards 5' ut

Trityl Group: Off Synthesis Scale: 0.2 Micromole Scale

Date Received:
Date Synthesised:
Number of Day(s) in the System: 4

If you have any problems, contact the Biopolymers Facility
Your assigned System Id number is 9076
Thank you for using the HHMI Biopolymer Facility.

$A_{260} = .217$

46/954

BIOMEDICAL RESEARCH CORE FACILITIES
DNA SYNTHESIS CORE 2562 MSRB II 764-1461

Synthesis Request Sheet

FACILITY USE ONLY:

Sequence #

3445 B

Applied Biosystems G 404052

Column

Date Synthesized

SAS

BB

Date Submitted:

Requestor: Kelly

Phone Number: 74756

Account Number: 921099

P.I. Name: LOWE

Billing Dept.: HHMI

Sequence Length: 20

Synthesis Scale: 0.2 umole

Trityl Group: No

HPLC Purify: No

Thio-Chemistry: No

Center Membership: None

Center/Project Related Research: No

SEQUENCE, 5' -> 3', IN TRIPLETS (* PLEASE START WITH A TRIPLET *)

CTA GCT GGT CAT TTC TAG GG

User Comments:

ft7-1

Comments to Core Facility:

DNA SEQUENCE 1

NUMBER OF BASES: 20

BASES USED: A=3 C=4 G=6 T=7 X=0

DALTONS: 5115

TIME:

DATE:

5' -> CTA GCT GGT CAT TTC TAG GG < 3'

Report for Synthetic Oligonucleotide

Date:

Investigator: LOWE
Individual User: Gersten

System Id: 8953

Product Information

Length: 20

Oligonucleotide Sequence:
TCA ATT CCC TCT TTG AGC AG

Comments:
104 phage from 8903 primer towards 3' end

Trityl Group: Off Synthesis Scale: 0.2 Micromole Scale

Date Received:
Date Synthesised:
Number of Day(s) in the System: 3

If you have any problems, contact the Biopolymers Facility
Your assigned System Id number is 8953
Thank you for using the HHMI Biopolymer Facility.

$A_{260} = 1.290$

38ul / 965ul

Report for Synthetic Oligonucleotide

Date:

Investigator: LOWE
Individual User: Gersten

System Id: 8952

Product Information

Length: 20

Oligonucleotide Sequence:
ATC AAC CAC TAT CCA ATC CT

Comments:

104 phage from primer 8903 towards 5' end

Trityl Group: Off

Synthesis Scale: 0.2 Micromole Scale

Date Received:

Date Synthesised:

Number of Day(s) in the System: 3

If you have any problems, contact the Biopolymers Facility
Your assigned System Id number is 8952
Thank you for using the HHMI Biopolymer Facility.

$A_{260} = 0.290$

7522 (965ul)

Report for Synthetic Oligonucleotide

Date:

Investigator: LOWE
Individual User: Gersten

System Id: 8904

Product Information

Length: 20

Oligonucleotide Sequence:
TGA CAA TTC CAG AAG GCT CC

Comments:

104 phage from primer 8874 towards 3' end of gene

Trityl Group: Off

Synthesis Scale: 0.2 Micromole Scale

Date Received:

Date Synthesized:

Number of Day(s) in the System: 3

If you have any problems, contact the Biopolymers Facility
Your assigned System Id number is 8904
Thank you for using the HHMI Biopolymer Facility.

$A_{260} = .272$

37 ml / 963

Report for Synthetic Oligonucleotide

Date:

Investigator: LOWE
Individual User: Gersten

System Id: 8903

Product Information

Length: 20

Oligonucleotide Sequence:
GGC CAG GCA CTC ACC AAT AC

Comments:

104 phage from primer 8874 towards 5' end of gene

Trityl Group: Off

Synthesis Scale: 0.2 Micromole Scale

Date Received:

Date Synthesised:

Number of Day(s) in the System: 3

If you have any problems, contact the Biopolymers Facility
Your assigned System Id number is 8903
Thank you for using the HHMI Biopolymer Facility.

$A_{260} = .292$

35 μ l / 965

Report for Synthetic Oligonucleotide

Date:

Investigator: LOWE
Individual User: Gersten

System Id: 8902

Product Information

Length: 20

Oligonucleotide Sequence:
TTA TTC TGC TTC AGG GTA CC

Comments:

104 phage from primer 8874 towards 3' end of gene

Trityl Group: Off

Synthesis Scale: 0.2 Micromole Scale

Date Received:

Date Synthesised:

Number of Day(s) in the System: 3

If you have any problems, contact the Biopolymers Facility
Your assigned System Id number is 8902
Thank you for using the HHMI Biopolymer Facility.

A260 = .297

342 / 966

Report for Synthetic Oligonucleotide

Date:

Investigator: LOWE
Individual User: Gersten

System Id: 8875

Product Information

Length: 20

Oligonucleotide Sequence:
ATC TGC ACT GGC CTT TCA CC

Comments:

104 phage from primer 8850 towards 3' end of gene

Trityl Group: Off

Synthesis Scale: 0.2 Micromole Scale

Date Received:

Date Synthesised:

Number of Day(s) in the System: 2

If you have any problems, contact the Biopolymers Facility
Your assigned System Id number is 8875
Thank you for using the HHMI Biopolymer Facility.

$A_{260} = 0.300$


33 μ l / 967 μ l

11 G/C

BIOMEDICAL RESEARCH CORE FACILITIES
DNA SYNTHESIS CORE 2562 MSRB II 764-1461

9 G/K
4 AT

Synthesis Request Sheet

FACILITY USE ONLY: Sequence # 524 B
Column  C 416455
Date Synthesized *D.G.*
Today's Date: Requestor: Gersten Sequence Length: 41
P.I. Name: LOWE Synthesis Scale: 0.2 umole
Billing Dept.: HHMI Tritvl Group: ☐ On ☒ Off
Phone Number: 7-4778 Thio-Chemistry: ☐ Yes ☒ No
Account Number: 921099

SEQUENCE, 5' → 3', IN TRIPLETS (* PLEASE START WITH A TRIPLET *)

GGC CGG ATC CCA CCA TCC TTA TCT GGC ACT GGC CTT TCA CC

User Comments:

phage 104 PCR primer (FOR AB) from nt 282

Comments to Core Facility:

- 394 Synthesis Setup Listing - (Version 1.01)

Column 4

Run ID :
Cycle : Cyc01 user
End Proc: End CE (DMT = Off)
Sequence: 624B

Total bases = 41

A= 6, G= 8, C= 17, T= 10, S= 0, 6= 0, 7= 0, 8= 0
(mixed bases= 0)

MW: 13246.2

✓ 5' → GGC CGG ATC CCA CCA TCC TTA TCT GGC ACT GGC CTT TCA
CC <3'

$A_{260} = .505$

~~200~~ 250 μ l 175 μ l

Report for Synthetic Oligonucleotide

Date:

Investigator: LOWE
Individual User: Gersten

System Id: 8874

Product Information

Length: 20

Oligonucleotide Sequence:
TGG TGA GTG TGG ACT GAG GC

Comments:

104 phage from primer 8850 towards 5' end of gene

Trityl Group: Off

Synthesis Scale: 0.2 Micromole Scale

Date Received:

Date Synthesised:

Number of Day(s) in the System: 2

If you have any problems, contact the Biopolymers Facility
Your assigned System Id number is 8874
Thank you for using the HHMI Biopolymer Facility.

$A_{260} = .300$

33rd / 967

Report for Synthetic Oligonucleotide

Date:

Investigator: LOWE

System Id: 8867

Individual User: Gersten

Product Information

Length: 20

Oligonucleotide Sequence:

GCT AGC AGG CTC CCG TTA GC

Comments:

104phage from 8770primer (b sequence) towards 5' end of gene

Trityl Group: Off

Synthesis Scale: 0.2 Micromole Scale

Date Received:

Date Synthesised:

Number of Day(s) in the System: 3

If you have any problems, contact the Biopolymers Facility

Your assigned System Id number is 8867

Thank you for using the HHMI Biopolymer Facility.

$$A_{260} = .259$$

38ul / 962

Report for Synthetic Oligonucleotide

Date:

Investigator: LOWE
Individual User: Gersten

System Id: 8851

Product Information

Length: 20

Oligonucleotide Sequence:
CCT TGG GTC TGG GCC TCC AT

Comments:

104 phage from 8770 primer towards 3' end of gene

Trityl Group: Off

Synthesis Scale: 0.2 Micromole Scale

Date Received:

Date Synthesised:

Number of Day(s) in the System: 1

If you have any problems, contact the Biopolymers Facility
Your assigned System Id number is. 8851
Thank you for using the HHMI Biopolymer Facility.

$A_{260} = 0.281$

36 μ l / 1

136K

Report for Synthetic Oligonucleotide

Date:

Investigator: LOWE
Individual User: Gersten

System Id: 8850

Product Information

Length: 20

Oligonucleotide Sequence:
AAG CGA TAG AGA CCA TGG GT

Comments:

104 phage from 8770 primer towards 5' end of gene

Trityl Group: Off

Synthesis Scale: 0.2 Micromole Scale

Date Received:

Date Synthesised:

Number of Day(s) in the System: 1

If you have any problems, contact the Biopolymers Facility
Your assigned System Id number is 8850
Thank you for using the HHMI Biopolymer Facility.

$$A_{260} = .264$$

39 μ l / 962

Report for Synthetic Oligonucleotide

Date:

Investigator: LOWE
Individual User: Gersten

System Id: 8771

Product Information

Length: 20

Oligonucleotide Sequence:
GSC CCA CAT CCC CAC TAC CG

Comments:

104 phage from 8715 sequence towards 3' end (towards rp2 primer sequ

Trityl Group: Off Synthesis Scale: 0.2 Micromole Scale

Date Received:

Date Synthesised:

Number of Day(s) in the System: 3

If you have any problems, contact the Biopolymers Facility
Your assigned System Id number is 8771
Thank you for using the HHMI Biopolymer Facility.

$A_{260} = 0.255$

39 μ l
961

Report for Synthetic Oligonucleotide

Date:

Investigator: LOWE
Individual User: Gersten

System Id: 8852

Product Information

Length: 20

Oligonucleotide Sequence:
CAC GCT GCT GCC GCT CCT GG

Comments:

104 phage from 8715 primer towards 5' end of gene (replace primer 877)

Trityl Group: Off Synthesis Scale: 0.2 Micromole Scale

Date Received:

Date Synthesised:

Number of Day(s) in the System: 1

If you have any problems, contact the Biopolymers Facility
Your assigned System Id number is 8852
Thank you for using the HHMI Biopolymer Facility.

$A_{260} = .265$

38ul / 962

Report for Synthetic Oligonucleotide

Date:

Investigator: LOWE
Individual User: Gersten

System Id: 8714

Product Information

Length: 20

Oligonucleotide Sequence:
GCA TCG BGA CTA CAT CAC TG

Comments:

104pst from rp2 sequence towards the 3' end

Trityl Group: Off

Synthesis Scale: 0.2 Micromole Scale

Date Received:

Date Synthesised:

Number of Day(s) in the System: 3

If you have any problems, contact the Biopolymers Facility
Your assigned System Id number is 8714
Thank you for using the HHMI Biopolymer Facility.

$A_{260} = .266$

38ul oligo
962ul H_2O

Report for Synthetic Oligonucleotide

Date: 10

Investigator: LDWE
Individual User: Gersten

System Id: 8715

Product Information

Length: 20

Oligonucleotide Sequence:
AGC CCC AGG CAT TGC GCC AG

Comments:

104pst from rp2 primer towards the 5' end

Trityl Group: Off

Synthesis Scale: 0.2 Micromole Scale

Date Received:

Date Synthesised:

Number of Day(s) in the System: 3

If you have any problems, contact the Biopolymers Facility
Your assigned System Id number is 8715
Thank you for using the HHMI Biopolymer Facility.

$A_{260} = 0.297$

33ul *ligo*
967ul $H_{2}O$

Report for Synthetic Oligonucleotide

Date:

Investigator: LOWE
Individual User: Gersten

System Id: 8848

Product Information

Length: 20

Oligonucleotide Sequence:
AAC TGG CTG TCT TCC TCG TC

Comments:

104phage from primer 8714 towards 3' end

Trityl Group: Off

Synthesis Scale: 0.2 Micromole Scale

Date Received:

Date Synthesised:

Number of Day(s) in the System: 1

If you have any problems, contact the Biopolymers Facility
Your assigned System Id number is 8848
Thank you for using the HHMI Biopolymer Facility.

$A_{260} = .299$

Report for Synthetic Oligonucleotide

Date:

Investigator: LOWE
Individual User: Gersten

System Id: 8849

Product Information

Length: 20

Oligonucleotide Sequence:
CAC GAT AAC GAC TCT CAT TC

Comments:

104 phage from primer B714 towards 5' end

Trityl Group: Off Synthesis Scale: 0.2 Micromole Scale

Date Received:

Date Synthesised:

Number of Day(s) in the System: 1

If you have any problems, contact the Biopolymers Facility
Your assigned System Id number is 8849
Thank you for using the HHMI Biopolymer Facility.

$$A_{260} = .283$$

3542 / 965

Report for Synthetic Oligonucleotide

Date:

Investigator: LOWE
Individual User: Gersten

System Id: 8868

Product Information

Length: 20

Oligonucleotide Sequence:
CTG GAG GGA AGC GCT TCT GC

Comments:

104 phage from 8714 (a sequence) towards 3' end of gene

Trityl Group: Off Synthesis Scale: 0.2 Micromole Scale

Date Received:

Date Synthesised:

Number of Day(s) in the System: 3

If you have any problems, contact the Biopolymers Facility
Your assigned System Id number is 8868
Thank you for using the HHMI Biopolymer Facility.

$T_m = 60$

$A_{260} = 0.330$

30 ml / 970

Report for Synthetic Oligonucleotide

Date:

Investigator: LOWE
Individual User: Gersten

System Id: 8876

Product Information

Length: 20

Oligonucleotide Sequence:
CAA GTA AGG GTA GCG GGC AC

Comments:

104 phage from primer 8848 towards 5' end of gene

Trityl Group: Off

Synthesis Scale: 0.2 Micromole Scale

Date Received:

Date Synthesised:

Number of Day(s) in the System: 2

If you have any problems, contact the Biopolymers Facility
Your assigned System Id number is 8876
Thank you for using the HHMI Biopolymer Facility.

$A_{260} = 0.287$

35ul / 965ul

BIOMEDICAL RESEARCH CORE FACILITIES
DNA SYNTHESIS CORE 2562 MSRB II 764-1461

Synthesis Request Sheet

FACILITY USE ONLY: Sequence # 625 B
Column **dbi** **407370**
Date Synthesized **D.G.**

Today's Date: Requestor: Gersten Sequence Length: 43
P.I. Name: LOWE Synthesis Scale: 0.2 umole
Billing Dept.: HHMI Trityl Group: ___On ___X___ Off
Phone Number: 7-4778 Thio-Chemistry: ___Yes ___X___ No
Account Number: 921099

SEQUENCE, 5'→ 3', IN TRIPLETS (* PLEASE START WITH A TRIFLET *)

GCG CGG ATC CTC ATC AAG CCT GGA ACC AGC TTT CAA GGT CTT C

User Comments:
104 phage PCR (for ab) from stop codon

Comments to Core Facility:

COLUMN 1 SET-UP
VERSION 2.01

USER_NAME:
CYCLES USED: 55CEAF31- 1
ENDING METHOD: Trityl OFF, Auto
ENDING PROCEDURE: DEPCRE03
SEQUENCE NAME: 625B
SEQUENCE LENGTH: 43
DATE:
TIME:
COMMENT:

✓ 5' GCG CGG ATC CTC ATC AAG CCT GGA ACC AGC TTT CAA

GGT CTT C -3'

$A_{260} = 0.662$

19 ul / 81 ul

Report for Synthetic Oligonucleotide

Date:

Investigator: LOWE
Individual User: Gersten

System Id: 8905

Product Information

Length: 20

Oligonucleotide Sequence:
CAG GAA TTC AGG ATA TAA GG

Comments:

104 phage from primer 886B towards 3' end of gene

Trityl Group: Off

Synthesis Scale: 0.2 Micromole Scale

Date Received:

Date Synthesised:

Number of Day(s) in the System: 3

If you have any problems, contact the Biopolymers Facility
Your assigned System Id number is 8905
Thank you for using the HHMI Biopolymer Facility.

$A_{260} = 0.312$

322/968

Report for Synthetic Oligonucleotide

Date:

Investigator: LONE
Individual User: Gersten

System Id: 8877

Product Information

Length: 20

Oligonucleotide Sequence:
GGT AGT GCC ATG GTG ACC AA

Comments:

104 phage from primer 8848 towards 5' end of gene

Trityl Group: Off

Synthesis Scale: 0.2 Micromole Scale

Date Received:

Date Synthesised:

Number of Day(s) in the System: 2

If you have any problems, contact the Biopolymers Facility
Your assigned System Id number is 8877
Thank you for using the HHMI Biopolymer Facility.

$$A_{260} = .318$$

31ul / 969ul

Report for Synthetic Oligonucleotide

Date:

Investigator: LOWE
Individual User: Gersten

System Id: 8954

Product Information

Length: 20

Oligonucleotide Sequence:
AGG TTG CAG ATG CAC CCT CT

Comments:

104 phage from primer 8905 towards 3' ut

Trityl Group: Off

Synthesis Scale: 0.2 Micromole Scale

Date Received:

Date Synthesised:

Number of Day(s) in the System: 4

If you have any problems, contact the Biopolymers Facility
Your assigned System Id number is 8954
Thank you for using the HHMI Biopolymer Facility.

$A_{260} = .272$

37ul / 963ul

Report for Synthetic Oligonucleotide

Date:

Investigator: LOWE

System Id: 8967

Individual User: Gersten

Product Information

Length: 20

Oligonucleotide Sequence:

GTA CTA GAG GGT GCA TCT GC

44+

Comments:

104 phage from rp2 primer (sac insert) towards 5' end of gene

Trityl Group: Off

Synthesis Scale: 0.2 Micromole Scale

Date Received:

Date Synthesised:

Number of Day(s) in the System: 5

If you have any problems, contact the Biopolymers Facility
Your assigned System id number is 8967
Thank you for using the HHMI Biopolymer Facility.

$T_a = 56$

use 104₂₀₀ 1189

$A_{260} = .230$

442/956

Report for Synthetic Oligonucleotide

Date:

Investigator: LOWE
Individual User: Gersten

System Id: 8713

Product Information

Length: 20

Oligonucleotide Sequence:
ACC ACT CAA GCA AGG CTC TC

Comments:
104pstt7 towards rp2 primer

Trityl Group: Off Synthesis Scale: 0.2 Micromole Scale

Date Received:
Date Synthesised:
Number of Day(s) in the System: 3

If you have any problems, contact the Biopolymers Facility
Your assigned System Id number is 8713
Thank you for using the HHMI Biopolymer Facility.

$A_{260} = .327$

3122 oligo
96922 H₂O

Primers used to sequence the mouse FuctVII genomic sequence in their order of appearance in the sequence.

3242
1088B
9392A
1042
8660A
9393A
986B
672B
887B
8993
671B
3511B
945B
715B
2931
2932
8661A
911B
9077
9076
3445B
8953
8952
8904
8903
8902
8875
624B
8874
8867
8851
8850
8771
8852
8714
8715
8848
8849
8868
8876
625B
8905
8877
8954
8967
8713

EXHIBIT E: Mouse FucT-VII gene, from phage 104, annotated with DNA sequencing primers used to sequence the phage, with start and stop codons, and with relevant restriction sites. Mouse genomic DNA sequence displayed from position 25,277,900 to 25,282,400 containing the coding sequence for the mouse FucT-VII gene

```

CTACCCCTGCT CTGGTTGGAC GAGGGTCCAC AAGGTCTCTT AGGCTGGGTA GAATAGAATG 60
GATGGGACGA GACCAACCTG TCCCAGGTT TCCAGAGAAA TCCAGCCCAT CTTATCTTAC

TGTGATCCTG ATCCCTGGAAC CCCAGATGTA AAGCTGGGTI TGGGTGCCCT TGTGAGTGAG 120
ACACTAGGAC TAGGACCTTG GGTCTACAT TTCGACCCAA ACCCACGGGA ACACCTCACTC

GAGGCCTGGT GAGGTGAGGT GGTATGTTGA GGTCCCCTGG CTTTCCCTTT GACTCATGAT 180
CTCCGGACCA CTCCACTCCA CCATACAACCT CCAGGGGACC GAAAGGAAA CTGAGTACTA

GTCTCACATT CCCCCACCC CCTTTTCCAT CCTGACCCCA TTTCTGAGCT AAATTTCCGA 240
CAGAGTGTA GGGGGGTGGG GGAAAAGGTA GGAATGGGGT AAAGACTCGA TTTAAAGGCT

ACTGACTCCT CAGTTGGCAA GTTCTCATGG TCAGGTGCCC TACAGTTAAC AGACCCCTGTG 300
TGACTGAGGA GTCAACCGTT CAAGAGTACC AGTCCACGGG ATGTCAAATTG TCTGGGACAC

GGACCTCCT CCAAAGTGAG CTGGCATGGG GAGGGGGTCA GTATAACAGC AAGGCAGATG 360
CCTGGGAGGA GGTTTGACTC GACCGTACCC CTCCCCCAGT CATATTGTCG TTCCGCTCTAC

TGGGGGAGGT TCCTTCAAAT CACCCAGGA AGGGAAGAGC ATGTGGGCGT GGGTGAGGCT 420
ACCCCTTCCA AGGAAGTTTA GGTGGGTCCT TCCCTTCTCG TACACCCGCA CCCACTCCGA
3242B

GGGGCAAAG CCCCAGCCAG CCTGGCGGCA CAAACAGGAA GGACAGCAGG CTCTGGCAGC 480
CCCCGTTTCC GGGGTGCGTC GGACCGCCGT GTTTGTCTCT CTTGTCTGTC GAGACCGTCG

CAGAAGCCTG TGGCCCCAAG CTGGCAGGAT GGCCCCCTTC CTGCGAGTCC CCCACAGCTC 540
GTCTTCGGAC ACCGGGGTTC GACCGTCTTA CCGGGGGAAG GACGCTCCAG GGGTGTTCGGA

TCTGGGTTC TGACACGAGA GAAGAGGTGG GGCGGGGTGA AGTGAACCTCT GAAGCCAAAA 600
AGACCCAAGG ACTGTGCTCT CTTCTCCACC CCGCCCCACT TCACCTTGAGA CTTCCGTTTTT

TGTGACTCTC CTGGGGTCAC CAGCTTGGGG AGAGGTGAAG AAAGATGCCG GGGCGGAAAC 660
ACACTGAGAG GACCCCAAGT GTCGAAACCC TCTCCACTTC TTTCTACGGC CCCGCTTTTG
EcoRI 1088B

AAAGGGGCAG ATATCACTAT GGTATCTTA CTAAGCACAG AGTAACTGAA AAAGCAAGGG 720
TTTCCCCGTC TATAGTGATA CCAATAGAAT GATTCTGTGC TCATTGACTT TTTCTGTCCC
9392A

TACCGTGCC CACCTCTGTC CCACCTTACG TTATACCTCA AACCAGCTAG ATAGTTTCTG 780
ATGGCGACGG GTGGAGCACG GGTGGAATGC AATATGAGT TTGGTCGATC TATCAAAGAC

ATGGCACCCA TACCTCTCCT TCCCCTTTAG GCATTCGCGA AGCTCTCCAC CACAATCTGG 840
TACCGTGGGT ATGGGAGGGA AGGGGAAATC CGTAACGCGT TCGAGAGGTT GTGTGTAGAC
1042B 8660B

AAGTTATACC CTGCGAGGGG ATGGGCAGGG CACTTCTGAG GTGCCAATCA GCCTGCATCT 900
TTCAATATGG GACGCTCCCC TACCGTCCCC GTGAAGACTC CACGGTTACT CGGACGTGAT
9393A

GCCTCTGCCC TGGCCATGGC ACTGCTGTCA GTTCTTGGT ACCTGTCTCA ACAGCAGCCT 960
CBGAGACGGG ACCGATACCG TGACGACAGT CAAAGAACCA TGGACAGAGT TGTCTGTCGA

TGTCACGTGA GACTATGGCT GGCAGTGGG GTGGGGGCGA GAATCCTAGA AGCACAGGAG 1020
ACAGTGCACT CTGATACCGA CCGCCACCCC CACCCCGCTC CTTAGGATCT TCGTGTCTCT

```

EXHIBIT E

	986B	672B				
TGACATAGGG	TCGGGTCCGG	CAGAGCGAAG	TGTAGGAAGT	GATCCCCAAA	GGGATGCTGG	1080
ACTGTATCCC	AGCCCGACCC	GTCTCGCTTC	ACATCCCTCA	CTAGGGGTTT	CCCTACGACC	
				SacI		
GGACGATCTG	GCCAACACTG	TCCTCCCAAT	CAAAACTCCC	AGTCTGGAGC	TCTGGGACAT	1140
CTGTCTAGAC	CGGTTGTGAC	AGGAGGGTAA	GTTTGTAGGG	TCAGACCTCG	AGACCTGTGA	
GGACAAGCCA	GGCCTGCTAT	TCTCCATACA	GGGCTCCATA	GTGCTCTGGC	CAGCAGAGTG	1200
CCTGTTCCGT	CCGGACGATA	AGAGGTATGT	CCCGAGGTAT	CACAGGCCGA	GTCTCTCTAC	
	8993				887B	
GGGGATCTGG	TGGGGATGGA	GGAAGCTTAG	CTAAAAGCTT	TGTATAGGCT	GAAGCTCTGA	1260
CCCTTAGACC	ACCCCTACCT	CCTTCGAATC	GATTTTCGAA	ACATATCCGA	CTTCGAGACT	
GTGACCTGTC	TGGGCCACCC	TACCCTGGTC	TGGGCTGGGT	CATTGCATCC	CCAGATTGGA	1320
CACCTGGGACG	ACCCGGTGGG	ATGGGACCAG	ACCCGACCCA	GTAACGTAGG	GGTCTAACCT	
AGGCTTGGTG	AGATGGAGAG	GAACCTTGGC	TACAAGCTAT	AGCTTTGCCC	ACCAGAGCCT	1380
TCCGAACCAC	TCTACCTCTC	CTTGGAAACG	ATGTTTCGATA	TCGAAACGGG	TGGTCTCGGA	
	3511B			671B		
GCTGGAGGGG	AATCAAAACAA	GCCTGGACCT	GAGGCTGGGA	CTAGCTTTCC	TGTTTCTGGA	1440
CGACCTCCCC	TTAGTTTGGT	CGACCTGGGA	CTCCGACCTC	GATCGAAAGG	ACAAAGACCT	
	Start codon					946B
GTGGATGCCA	ACCCCTGGCC	CACCAGCCTG	CCTGTCCACG	CCAGGGACAC	ACAGACTCCT	1500
CACCTACGGT	TGGGGGACGG	GTGGTCGGAC	GGACAGGTGC	GGTCCCTGTG	TGCTTGAGGA	
TCCCTTTCCA	GACTGGAAAG	CCCCCTCCTG	GGAGAGCAGG	AAGGAAGCAA	CCTGCAAACTC	1560
AGGGAAAGGT	CTGACCTTTC	GGGGGAGGAC	CCTCTCGTCC	TTCCTTCGTT	GGACGTTGAG	
	2931B					
TTCCAGCCCT	GGACCTTGGG	CTGAACCTAC	AGTTCAAGGT	TTGTATGCTC	ACAGGTCTTG	1620
AAGGTCGGGA	CCTGGAACCC	GACTTGGATG	TCAAGTTCCA	AACATACGAG	TGTCCAGAAC	
			2932B			
GCAGGGAAAG	ATAAGAAATC	CCAGGGCACC	CTCCCCCCCC	CCCCCAGTC	CACCTGCAGGT	1680
CGTCCCTTTC	TATTCTTAGG	GGTCCCGTGG	GAGGGGGGGG	GGGGGGTCAG	GTGACGTCCA	
AGCTCCTGGG	TCTGCCCTTC	AGGGCAAGTG	CTGACGCTCC	ATCAGACTGT	GATGGGGCCC	1740
TCGAGGACCC	AGACGGGAAG	TCCCGTTCAC	GACTGCGAGG	TAGTCTGACA	CTACCCCGGG	
			8661A			
TTTTCTGAGG	ATGACAATTC	TGAGAACAAG	GCATTTTTCT	AGAGGTGGCA	GAACAGCATT	1800
AAAAGACTCC	TACTGTTAAG	ACTCTTGTTT	CGTAAAAAGA	TCTCCACCGT	CTTGTCTGTA	
TTGTGATGCC	CGAGGATCTG	GGAGCACAGG	TCCAGCTTAA	TGAGGGATTG	GAGGAAGTGG	1860
AACACTACGG	GCTCCTAGAC	CCTCGTGTCC	AGGTCGAATT	ACTCCCTAAC	CTCTTCACCC	
		911B				
GTATCATCAT	TACAGGGAGG	GGCCTCTGTG	GCCTCCTGGG	AAAATGCGAT	TGCTCTCTTT	1920
CATAGTAGTA	ATGTCCCTTC	CCGGAGACAC	CCGAGGACCC	TTTTCAGCTA	ACGAGAGAAA	
				9077		
GGGTGGCCCTG	GGGTTGTGTG	GTGGGCAGAG	GACGGAGGTG	CTCATTTGGGG	GAAGGGATCA	1980
CCCACCGGAC	CCCAACACAC	CACCCGCTCT	CTGCCTCCAC	GAGTAACCCC	CTTCCCTAGT	
CTTCTGCTCA	GAGTGCTCGC	AAGGGCCTTT	CCTTTTCTCT	AAGGCAAGCA	GGCCTCCTCC	2040
GAAGACGAGT	CTCAGGACGG	TTCCCGGAAA	GGAAAAGGAC	TTCCGTTCTG	CCGAGAGGAG	
			9076		3445B	
TCCTCCTCTT	CCTCCTTCTC	CTCTTCTCTC	TCTTTCTCCA	TATGCCTAGC	TGGTCATTTC	2100
AGGAGGAGAA	GGAGGAAGAG	GAGAAGGAGG	AGAAAGAGGT	ATACGGATCG	ACCAGTAAAG	

EXHIBIT E

						8953	
TAGGGACCAG	CATGGTTGGG	AAGGGGGCCT	TGTCTTGGCC	TTCCTCTTGT	CTCAATTCCC	2160	
ATCCCTGGTC	GTACCAACCC	TTCCCCCGGA	ACAGAACCGG	AAGGAGAACA	GAGTTAAAGG		
TCTTTGAGCA	GAAGACGGGG	TGGGTGGGGT	AGGGTTGGAT	AGTGGTTGAT	GCCAAAGATT	2220	
AGAAACTCGT	CTTCTGCCCC	ACCCACCCCA	TCCCAACCTA	TCACCAACTA	CGGTTTCTAA		
GAAGGGGTAG	GGCGGGGCAG	AAGTGGGAAG	GTCCCTGGCT	TCCTCACCTT	GGTAGATGGT	2280	
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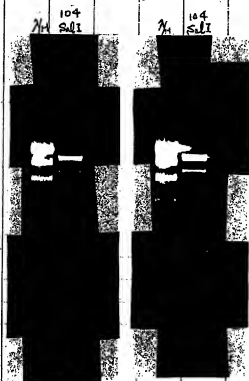
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Southern blot of mFT7 phage (104)

1 μ l 104 phage ($\sim 0.75 \mu$ g)
 ↓ Sal I digest
 ↓ 0.6 % agarose GE



© No Sal I site in insert DNA of 104-phage

20kb arm insert 2kb arm λ -FIX II

1a. 1 μ l 104 phage ($\sim 0.75 \mu$ g)
 ↓ EcoRI or Pst I digest
 ↓ cont. of NaCl adjust to 150 mM
 ↓ Sal I digest 0.1 %

2a. 7.5 μ l FVB mouse gDNA (15 μ g)
 ↓ EcoRI or Pst I digest 0.1 %

BLAST Basic Local Alignment Search ToolJob Title: lc|32071 (8970 letters)

•
•
•**BLASTN 2.2.17 (Aug-26-2007)**RID: HB3E6W8B013 Database: mouse build 37 RNA, reference and alternate assemblies 53,645 sequences;
5,338,491,926 total letters[Genome View](#)Show positions of the BLAST hits in the house mouse genome using the Entrez
Genomes MapViewer

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Distribution of 178 Blast Hits on the Query Sequence

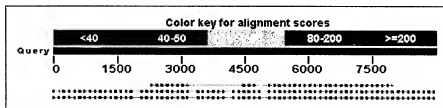


Exhibit G

Distance tree of results [NEW](#)Legend for links to other resources: [U](#) UniGene [E](#) GEO [G](#) Gene [S](#) Structure [M](#) Map ViewerSequences producing significant alignments:
(Click headers to sort columns)**Transcripts**

NW_013524.2	Mus musculus fucosyltransferase 7 (Fut7), mRNA	117	3969	23%	2e-22	100%	U E G S M
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Genomic sequences [show first]

NW_001030686.1	Mus musculus chromosome 2 genomic contig, alternate assembly (based on Celera assembly)	121	7907	47%	2e-23	100%	
NW_039206.7	Mus musculus chromosome 2 genomic contig, strain C57BL/6J	121	7962	48%	2e-23	100%	



Search Nucleotide

for

Limits

Preview/Index

History

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Details

Display GenBank

Show 5

Send to

Hide:

☐ sequence☐ all but gene, CDS and mRNA features

Range: from begin

to end

☐ Reverse complemented strandFeatures: ☒ STS ☒ Exon☐ 1: NM_013524. Reports Mus musculus fuco...[gi:118129912]

Links

Comment Features Sequence

LOCUS NM_013524 2185 bp mRNA linear ROD 03-SEP-2007

DEFINITION Mus musculus fucosyltransferase 7 (Fut7), mRNA.

ACCESSION NM_013524

VERSION NM_013524.2 GI:118129912

KEYWORDS .

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 2185)

AUTHORS Hiraoka,N., Petryniak,B., Kawashima,H., Mitoma,J., Akama,T.O.,
Fukuda,M.N., Lowe,J.B. and Fukuda,M.

TITLE Significant decrease in alpha1,3-linked fucose in association with
increase in 6-sulfated N-acetylglucosamine in peripheral lymph node
addressin of FucT-VII-deficient mice exhibiting diminished
lymphocyte homing

JOURNAL Glycobiology 17 (3), 277-293 (2007)

PUBMED 1712261

REMARK GeneRIF: Keratan sulfate sulfotransferase competes with FucT-VII
for the same acceptor substrate and downregulates the synthesis of
L-selectin ligand by inhibiting alpha1,3-fucosylation.

REFERENCE 2 (bases 1 to 2185)

AUTHORS Laubli,H., Stevenson,J.L., Varki,A., Varki,N.M. and Borsig,L.

TITLE L-selectin facilitation of metastasis involves temporal induction
of Fut7-dependent ligands at sites of tumor cell arrest

JOURNAL Cancer Res. 66 (3), 1536-1542 (2006)

PUBMED 16452210

REFERENCE 3 (bases 1 to 2185)

AUTHORS Chen,S., Kawashima,H., Lowe,J.B., Lanier,L.L. and Fukuda,M.

TITLE Suppression of tumor formation in lymph nodes by
L-selectin-mediated natural killer cell recruitment

JOURNAL J. Exp. Med. 202 (12), 1679-1689 (2005)

PUBMED 16352740

REFERENCE 4 (bases 1 to 2185)

AUTHORS Eom,H.S., Rubio,M.T., Means,T.K., Luster,A.D. and Sykes,M.

TITLE T-cell P/E-selectin ligand alpha(1,3)fucosylation is not required
for graft-vs-host disease induction

JOURNAL Exp. Hematol. 33 (12), 1564-1573 (2005)

PUBMED 16338500

REFERENCE 5 (bases 1 to 2185)

AUTHORS Satoh,T., Kanai,Y., Wu,M.H., Yokozeki,H., Kannagi,R., Lowe,J.B. and
Nishioka,K.

TITLE Synthesis of (alpha)(1,3) fucosyltransferases IV- and VII-dependent
eosinophil selectin ligand and recruitment to the skin

JOURNAL Am. J. Pathol. 167 (3), 787-796 (2005)

PUBMED 16121157

REMARK GeneRIF: FT-IV and FT-VII are both important contributors to
selectin-dependent eosinophil recruitment to the skin and may
represent therapeutic targets for treating diseases in which
eosinophil recruitment contributes to pathophysiology.

REFERENCE 6 (bases 1 to 2185)
 AUTHORS Homeister,J.W., Thall,A.D., Petryniak,B., Maly,P., Rogers,C.E., Smith,P.L., Kelly,R.J., Gersten,K.M., Askari,S.W., Cheng,G., Smithson,G., Marks,R.M., Misra,A.K., Hinds Gaul,O., von Andrian,U.H. and Lowe,J.B.
 TITLE The alpha(1,3)fucosyltransferases FucT-IV and FucT-VII exert collaborative control over selectin-dependent leukocyte recruitment and lymphocyte homing
 JOURNAL Immunity 15 (1), 115-126 (2001)
 PUBMED 11485743

REFERENCE 7 (bases 1 to 2185)
 AUTHORS Beck,P.L., Xavier,R., Lu,N., Nanda,N.N., Dinanuer,M., Podolsky,D.K. and Seed,B.
 TITLE Mechanisms of NSAID-induced gastrointestinal injury defined using mutant mice
 JOURNAL Gastroenterology 119 (3), 699-705 (2000)
 PUBMED 10982764

REFERENCE 8 (bases 1 to 2185)
 AUTHORS Weninger,W., Ulfman,L.H., Cheng,G., Souchkova,N., Quackenbush,E.J., Lowe,J.B. and von Andrian,U.H.
 TITLE Specialized contributions by alpha(1,3)-fucosyltransferase-IV and FucT-VII during leukocyte rolling in dermal microvessels
 JOURNAL Immunity 12 (6), 665-676 (2000)
 PUBMED 10894166

REFERENCE 9 (bases 1 to 2185)
 AUTHORS Maly,P., Thall,A., Petryniak,B., Rogers,C.E., Smith,P.L., Marks,R.M., Kelly,R.J., Gersten,K.M., Cheng,G., Saunders,T.L., Camper,S.A., Camphausen,R.T., Sullivan,F.X., Isogai,Y., Hinds Gaul,O., von Andrian,U.H. and Lowe,J.B.
 TITLE The alpha(1,3)fucosyltransferase Fuc-TVII controls leukocyte trafficking through an essential role in L-, E-, and P-selectin ligand biosynthesis
 JOURNAL Cell 86 (4), 643-653 (1996)
 PUBMED 8752218

REFERENCE 10 (bases 1 to 2185)
 AUTHORS Smith,P.L., Gersten,K.M., Petryniak,B., Kelly,R.J., Rogers,C., Natsuka,Y., Alford,J.A. III, Scheidegger,E.P., Natsuka,S. and Lowe,J.B.
 TITLE Expression of the alpha(1,3)fucosyltransferase Fuc-TVII in lymphoid aggregate high endothelial venules correlates with expression of L-selectin ligands
 JOURNAL J. Biol. Chem. 271 (14), 8250-8259 (1996)
 PUBMED 8626519

COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final NCBI review. The reference sequence was derived from [AL732557.4](#). On Nov 17, 2006 this sequence version replaced [gi:7305072](#).

Sequence Note: The RefSeq transcript and protein were derived from genomic sequence to make the sequence consistent with the reference genome assembly. The genomic coordinates used for the transcript record were based on alignments.

Publication Note: This RefSeq record includes a subset of the publications that are available for this gene. Please see the Entrez Gene record to access additional publications.

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Aug 28 2007 16:55:42



Blast 2 Sequences results

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Entrez

BLAST

OMIM

Taxonomy

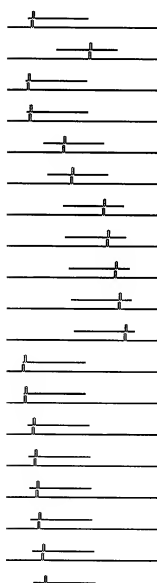
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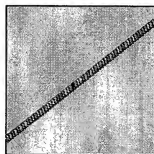
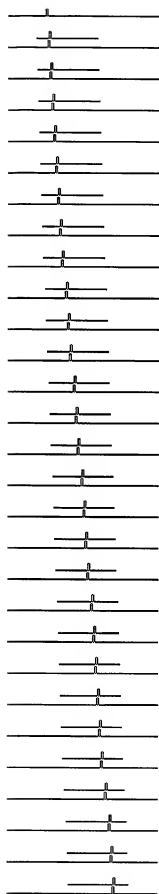
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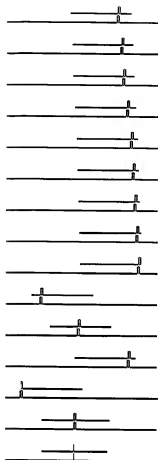
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1

NOTE:Bitscore and expect value are calculated based on the size of the nr database.

NOTE:If protein translation is reversed, please repeat the search with reverse strand of the query sequence.

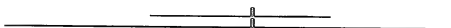


Score = 125 bits (65), Expect = 1e-24
 Identities = 65/65 (100%), Gaps = 0/65 (0%)
 Strand=Plus/Plus

```

Query  272  TACCGCTGCCACCTCGTGCCACCTTACGTTATACCTCAAACCAGCTAGATAGTTTCTG  331
          |||||||
Sbjct  1441  TACCGCTGCCACCTCGTGCCACCTTACGTTATACCTCAAACCAGCTAGATAGTTTCTG  1500

Query  332  ATGGC  336
          |||||
Sbjct  1501  ATGGC  1505
  
```

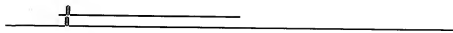


Score = 121 bits (63), Expect = 2e-23
 Identities = 63/63 (100%), Gaps = 0/63 (0%)
 Strand=Plus/Plus

```

Query  2012  GTGTCCTTGAGCCTAGGGTGACAGGGCCTCTCCTTTTTTTTATCTGCTTCAGGGTAC  2071
          |||||||
Sbjct  4921  GTGTCCTTGAGCCTAGGGTGACAGGGCCTCTCCTTTTTTTTATCTGCTTCAGGGTAC  4980
  
```

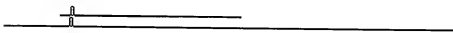
Query 2072 CAC 2074
 |||
 Sbjct 4981 CAC 4983



Score = 117 bits (61), Expect = 2e-22
 Identities = 61/61 (100%), Gaps = 0/61 (0%)
 Strand=Plus/Plus

Query 152 TGTGACTCTCTGGGGTCACCAGCTTGGGGAGAGGTGAAGAAAGATGCCGGGCGGAAAC 211
 |||
 Sbjct 1201 TGTGACTCTCTGGGGTCACCAGCTTGGGGAGAGGTGAAGAAAGATGCCGGGCGGAAAC 1260

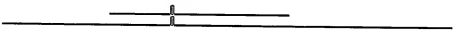
Query 212 A 212
 |
 Sbjct 1261 A 1261



Score = 117 bits (61), Expect = 2e-22
 Identities = 61/61 (100%), Gaps = 0/61 (0%)
 Strand=Plus/Plus

Query 212 AAAGGGGCAGATATCACTATGGTTATCTTACTAAGCACAGAGTAAGTGAAGCAAGGG 271
 |||
 Sbjct 1321 AAAGGGGCAGATATCACTATGGTTATCTTACTAAGCACAGAGTAAGTGAAGCAAGGG 1380

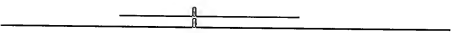
Query 272 T 272
 |
 Sbjct 1381 T 1381



Score = 117 bits (61), Expect = 2e-22
 Identities = 61/61 (100%), Gaps = 0/61 (0%)
 Strand=Plus/Plus

Query 1232 AGCTCCTGGGTCTGCCCTTCAGGGCAAGTGCTGACGCTCCATCAGACTGTGATGGGGCCC 1291
 |||
 Sbjct 3361 AGCTCCTGGGTCTGCCCTTCAGGGCAAGTGCTGACGCTCCATCAGACTGTGATGGGGCCC 3420

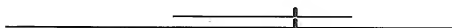
Query 1292 T 1292
 |
 Sbjct 3421 T 3421



Score = 117 bits (61), Expect = 2e-22
 Identities = 61/61 (100%), Gaps = 0/61 (0%)
 Strand=Plus/Plus

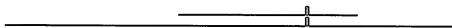
Query 1472 CGGTGGCCTGGGGTTGTGTGGTGGGCAGAGGACGGAGGTGCTCATTTGGGGGAAGGGATCA 1531
 |||

Sbjct 3841 GGGTGGCCTGGGGTTCTGTGGTGGGCAGAGGACGAGGTGCTCATTTGGGGGAAGGGATCA 3900
 Query 1532 C 1532
 |
 Sbjct 3901 C 3901



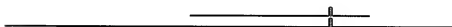
Score = 117 bits (61), Expect = 2e-22
 Identities = 61/61 (100%), Gaps = 0/61 (0%)
 Strand=Plus/Plus

Query 2432 ACCCATGGTCTCCATCGCTTCGGGGGCATCTTCACTGGGTGCTGAGCTATCGGCGTGTAT 2491
 |
 Sbjct 5761 ACCCATGGTCTCCATCGCTTCGGGGGCATCTTCACTGGGTGCTGAGCTATCGGCGTGTAT 5820
 Query 2492 T 2492
 |
 Sbjct 5821 T 5821



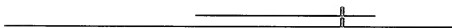
Score = 117 bits (61), Expect = 2e-22
 Identities = 61/61 (100%), Gaps = 0/61 (0%)
 Strand=Plus/Plus

Query 2552 CCGGCCAAAAGCAGGATGGCTGCTGGGTGATCAGCAATTTCCAGGAGCGGCAGCAGCGT 2611
 |
 Sbjct 6001 CCGGCCAAAAGCAGGATGGCTGCTGGGTGATCAGCAATTTCCAGGAGCGGCAGCAGCGT 6060
 Query 2612 G 2612
 |
 Sbjct 6061 G 6061



Score = 117 bits (61), Expect = 2e-22
 Identities = 61/61 (100%), Gaps = 0/61 (0%)
 Strand=Plus/Plus

Query 2792 GCGGCTGGTGTGTACCCGTGGCGCTGGGACCTCCTCGGGCCACCTACGAGGCTTTTGTG 2851
 |
 Sbjct 6481 GCGGCTGGTGTGTGTACCCGTGGCGCTGGGACCTCCTCGGGCCACCTACGAGGCTTTTGTG 6540
 Query 2852 C 2852
 |
 Sbjct 6541 C 6541



Score = 117 bits (61), Expect = 2e-22
 Identities = 61/61 (100%), Gaps = 0/61 (0%)
 Strand=Plus/Plus

Query 2912 CTCGTACGATGAATGAGAGTCGTTATCGTGGCTCTTTGCTTGGCGAGACCGGCTCCGT 2971

```

          |||
Sbjct  6721  CTCGTCAGCATGAATGAGAGTCGTATCGTGGCTTCTTTGCTTGGCGAGACCGGCTCCGT 6780
Query  2972  G 2972
          |
Sbjct  6781  G 6781

```

Score = 117 bits (61), Expect = 2e-22
 Identities = 61/61 (100%), Gaps = 0/61 (0%)
 Strand=Plus/Plus

```

Query  3092  GCTGGGAGAGGCTGGATGGGTGGGAGACTGATGTTGAACCAAGAGCTGGGCATCCAGG 3151
          |||
Sbjct  7081  GCTGGGAGAGGCTGGATGGGTGGGAGACTGATGTTGAACCAAGAGCTGGGCATCCAGG 7140
Query  3152  C 3152
          |
Sbjct  7141  C 7141

```

Score = 116 bits (60), Expect = 9e-22
 Identities = 60/60 (100%), Gaps = 0/60 (0%)
 Strand=Plus/Plus

```

Query  32     CAGAAGCCTGTGGCCCCAAGCTGGCAGGATGGCCCCCTTCCTGCAGGTCCCCACAGCCT 91
Sbjct  961    CAGAAGCCTGTGGCCCCAAGCTGGCAGGATGGCCCCCTTCCTGCAGGTCCCCACAGCCT 1020

```

Score = 116 bits (60), Expect = 9e-22
 Identities = 60/60 (100%), Gaps = 0/60 (0%)
 Strand=Plus/Plus

```

Query  92     TCTGGGTTCTTGACACGAGAGAAGAGTGGGGCGGGGTGAAGTGAACCTCTGAAGCCAAAA 151
Sbjct  1081   TCTGGGTTCTTGACACGAGAGAAGAGTGGGGCGGGGTGAAGTGAACCTCTGAAGCCAAAA 1140

```

Score = 116 bits (60), Expect = 9e-22
 Identities = 60/60 (100%), Gaps = 0/60 (0%)
 Strand=Plus/Plus

```

Query  332    ATGGCACCCATACCCTCCCTTCCCTTTAGGCATTGCGCAAGCTCTCCACCACAATCTGG 391
Sbjct  1561   ATGGCACCCATACCCTCCCTTCCCTTTAGGCATTGCGCAAGCTCTCCACCACAATCTGG 1620

```

Score = 116 bits (60), Expect = 9e-22
 Identities = 60/60 (100%), Gaps = 0/60 (0%)
 Strand=Plus/Plus

Query 392 AAGTTATACCCCTGCGAGGGGATGGGCAGGGCACCTTCTGAGGTGCCAATCAGCCTGCACCTC 451
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct 1681 AAGTTATACCCCTGCGAGGGGATGGGCAGGGCACCTTCTGAGGTGCCAATCAGCCTGCACCTC 1740



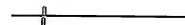
Score = 116 bits (60), Expect = 9e-22
 Identities = 60/60 (100%), Gaps = 0/60 (0%)
 Strand=Plus/Plus

Query 452 GCCTCTGCCCTGGCCATGGCAGCTGCTGTTCAGTTTCTTGGTACCTGTCTCAACAGCAGCCT 511
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct 1801 GCCTCTGCCCTGGCCATGGCAGCTGCTGTTCAGTTTCTTGGTACCTGTCTCAACAGCAGCCT 1860



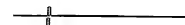
Score = 116 bits (60), Expect = 9e-22
 Identities = 60/60 (100%), Gaps = 0/60 (0%)
 Strand=Plus/Plus

Query 512 TGTCAAGTGAGACTATGGCTGGCGGTGGGGGTGGGGGCAGGAATCTAGAGCAGCAGGAG 571
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct 1921 TGTCAAGTGAGACTATGGCTGGCGGTGGGGGTGGGGGCAGGAATCTAGAGCAGCAGGAG 1980



Score = 116 bits (60), Expect = 9e-22
 Identities = 60/60 (100%), Gaps = 0/60 (0%)
 Strand=Plus/Plus

Query 632 GGACGATCTGGCCAACTGTCTCCATTCAAACCTCCAGCTCGGAGCTCTGGGACAT 691
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct 2161 GGACGATCTGGCCAACTGTCTCCATTCAAACCTCCAGCTCGGAGCTCTGGGACAT 2220



Score = 116 bits (60), Expect = 9e-22
 Identities = 60/60 (100%), Gaps = 0/60 (0%)
 Strand=Plus/Plus

Query 692 GGACAAGCCAGGCTGCTATTCTCCATACAGGGCTCCATAGTGTCTGGCTCAGCAGAGTG 751
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct 2281 GGACAAGCCAGGCTGCTATTCTCCATACAGGGCTCCATAGTGTCTGGCTCAGCAGAGTG 2340



Score = 116 bits (60), Expect = 9e-22
 Identities = 60/60 (100%), Gaps = 0/60 (0%)
 Strand=Plus/Plus

Query 752 GGGGATCTGGTGGGGATGGAGGAAGCTTAGCTAAAGCTTTGTATAGGCTGAAGCTCTGA 811
 |||
 Sbjct 2401 GGGGATCTGGTGGGGATGGAGGAAGCTTAGCTAAAGCTTTGTATAGGCTGAAGCTCTGA 2460



Score = 116 bits (60), Expect = 9e-22
 Identities = 60/60 (100%), Gaps = 0/60 (0%)
 Strand=Plus/Plus

Query 812 GTGACCTGCTGGGGCCACCCCTACCTGGCTCTGGGCTGGGTCATTGCATCCCCAGATTGGA 871
 |||
 Sbjct 2521 GTGACCTGCTGGGGCCACCCCTACCTGGCTCTGGGCTGGGTCATTGCATCCCCAGATTGGA 2580



Score = 116 bits (60), Expect = 9e-22
 Identities = 60/60 (100%), Gaps = 0/60 (0%)
 Strand=Plus/Plus

Query 872 AGGCTTGGTGAGATGGAGAGGAACCTTGGCTACAAGCTATAGCTTTGCCACCAAGAGCCT 931
 |||
 Sbjct 2641 AGGCTTGGTGAGATGGAGAGGAACCTTGGCTACAAGCTATAGCTTTGCCACCAAGAGCCT 2700



Score = 116 bits (60), Expect = 9e-22
 Identities = 60/60 (100%), Gaps = 0/60 (0%)
 Strand=Plus/Plus

Query 932 GCTGGAGGGGAATCAAAACAGCCTGGACCTGAGGCTGGGACTAGCTTTCTCTTTCTGGA 991
 |||
 Sbjct 2761 GCTGGAGGGGAATCAAAACAGCCTGGACCTGAGGCTGGGACTAGCTTTCTCTTTCTGGA 2820



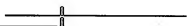
Score = 116 bits (60), Expect = 9e-22
 Identities = 60/60 (100%), Gaps = 0/60 (0%)
 Strand=Plus/Plus

Query 992 GTGGATGCCAACCCCTGCCCCAGGCTGCTGTCCAGGCCAGGGACACACAGACTCTCT 1051
 |||
 Sbjct 2881 GTGGATGCCAACCCCTGCCCCAGGCTGCTGTCCAGGCCAGGGACACACAGACTCTCT 2940



Score = 116 bits (60), Expect = 9e-22
Identities = 60/60 (100%), Gaps = 0/60 (0%)
Strand=Plus/Plus

Query 1052 TCCCTTTCCAGACTGGAAAGCCCCCTCTCTGGGAGAGCAGGAAGGAACCAACCTGCAACTC 1111
|||||
Sbjct 3001 TCCCTTTCCAGACTGGAAAGCCCCCTCTCTGGGAGAGCAGGAAGGAACCAACCTGCAACTC 3060



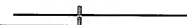
Score = 116 bits (60), Expect = 9e-22
Identities = 60/60 (100%), Gaps = 0/60 (0%)
Strand=Plus/Plus

Query 1112 TTCCAGCCCTGGACCTTGGGCTGAACCTACAGTTCAAGGTTTGTATGCTCACAGGTCCTTG 1171
|||||
Sbjct 3121 TTCCAGCCCTGGACCTTGGGCTGAACCTACAGTTCAAGGTTTGTATGCTCACAGGTCCTTG 3180



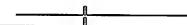
Score = 116 bits (60), Expect = 9e-22
Identities = 60/60 (100%), Gaps = 0/60 (0%)
Strand=Plus/Plus

Query 1172 GCAGGGAAAGATAAGAAATCCCCAGGGCACCTCCCCCGCCCCCAGTCCACTGCAGGT 1231
|||||
Sbjct 3241 GCAGGGAAAGATAAGAAATCCCCAGGGCACCTCCCCCGCCCCCAGTCCACTGCAGGT 3300



Score = 116 bits (60), Expect = 9e-22
Identities = 60/60 (100%), Gaps = 0/60 (0%)
Strand=Plus/Plus

Query 1292 TTTTCTGAGGATGACAATCTGAGAACCAAGGCATTTTCTAGAGGTGGCAGAACAGCATT 1351
|||||
Sbjct 3481 TTTTCTGAGGATGACAATCTGAGAACCAAGGCATTTTCTAGAGGTGGCAGAACAGCATT 3540



Score = 116 bits (60), Expect = 9e-22
Identities = 60/60 (100%), Gaps = 0/60 (0%)
Strand=Plus/Plus

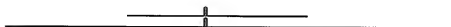
Query 1352 TTGTGATGCCCGAGGATCTGGGAGCACAGTCCAGCTTAATGAGGGATTGGAGGAAGTGG 1411
|||||
Sbjct 3601 TTGTGATGCCCGAGGATCTGGGAGCACAGTCCAGCTTAATGAGGGATTGGAGGAAGTGG 3660



```

Query  1412  GTATCATCATTACAGGGAGGGGCTCTGTGGCCTCCTGGGAAAATGCAGTTGCTCTCTTT 1471
          |||
Sbjct  3721  GTATCATCATTACAGGGAGGGGCTCTGTGGCCTCCTGGGAAAATGCAGTTGCTCTCTTT 3780

```



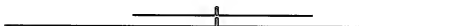
Query 1532 CTTCTGCTCAGAGTGCTCGCAAGGGCCCTTCCCTTTCTCTGAAGGCAAGCAGGCCTCCTCC 1591
Sbjct 3961 CTTCTGCTCAGAGTGCTCGCAAGGGCCCTTCCCTTTCTCTGAAGGCAAGCAGGCCTCCTCC 4020



```

Query    1592  TCCTCCTCTTCCTCCTTCTCCTCTTCCTCCTTTCTCCATATGCCTAGCTGGTCATTTC 1651
          |||||
Sbjct    4081  TCCTCCTCTTCCTCCTTCTCCTCTTCCTCCTTTCTCCATATGCCTAGCTGGTCATTTC 4140

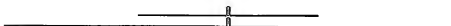
```



```

Query    1652  TAGGGACCAGCATGGTTGGGAAGGGGGCCTTGCTTGGCCCTCCTCTTGCTCAATTCCC 1711
          |||||
Sbjct    4201  TAGGGACCAGCATGGTTGGGAAGGGGGCCTTGCTTGGCCCTCCTCTTGCTCAATTCCC 4260

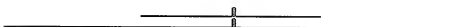
```



```

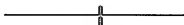
Query 1772 GAAGGGGTAGGGCGGGGCAGAAGTGGGAAGGTCCCTGGCTTCCTCACCTTGGTAGATGGT 1831
           |||
Sbjct 4441 GAAGGGGTAGGGCGGGGCAGAAGTGGGAAGGTCCCTGGCTTCCTCACCTTGGTAGATGGT 4500

```



Score = 116 bits (60), Expect = 9e-22
 Identities = 60/60 (100%), Gaps = 0/60 (0%)
 Strand=Plus/Plus

Query 1832 GAGGAGCCCCAGAGGTTGAGCTGAGCAGCAGCTGTGATTTTCAGGGTGCCTCTGTGGAGA 1891
 |||||||
 Sbjct 4561 GAGGAGCCCCAGAGGTTGAGCTGAGCAGCAGCTGTGATTTTCAGGGTGCCTCTGTGGAGA 4620



Score = 116 bits (60), Expect = 9e-22
 Identities = 60/60 (100%), Gaps = 0/60 (0%)
 Strand=Plus/Plus

Query 1892 GGCTGCTGTGATTTGAAAATCTTCTTTCCCTTGGTGACAATTCAGAGGCTCCAGATGAA 1951
 |||||||
 Sbjct 4681 GGCTGCTGTGATTTGAAAATCTTCTTTCCCTTGGTGACAATTCAGAGGCTCCAGATGAA 4740



Score = 116 bits (60), Expect = 9e-22
 Identities = 60/60 (100%), Gaps = 0/60 (0%)
 Strand=Plus/Plus

Query 1952 TTGTATTGGTGAGTGCCTGGCCCTTAAGCAGTCCAGCTGGGATGATGGGGATTTATGG 2011
 |||||||
 Sbjct 4801 TTGTATTGGTGAGTGCCTGGCCCTTAAGCAGTCCAGCTGGGATGATGGGGATTTATGG 4860



Score = 116 bits (60), Expect = 9e-22
 Identities = 60/60 (100%), Gaps = 0/60 (0%)
 Strand=Plus/Plus

Query 2072 CACCCACACAGGAGGCTGCGGGCCTGGGGCGGCCCTAGCTGGAGGAGCAACATTCATGTA 2131
 |||||||
 Sbjct 5041 CACCCACACAGGAGGCTGCGGGCCTGGGGCGGCCCTAGCTGGAGGAGCAACATTCATGTA 5100



Score = 116 bits (60), Expect = 9e-22
 Identities = 60/60 (100%), Gaps = 0/60 (0%)
 Strand=Plus/Plus

Query 2132 ATTTGGTTTTTCTGGCTGTGGGATCAGCTCCTGGAAGTGCCCTGTGCCTCAGTCCACA 2191
 |||||||
 Sbjct 5161 ATTTGGTTTTTCTGGCTGTGGGATCAGCTCCTGGAAGTGCCCTGTGCCTCAGTCCACA 5220



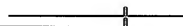
Score = 116 bits (60), Expect = 9e-22
 Identities = 60/60 (100%), Gaps = 0/60 (0%)
 Strand=Plus/Plus

Query 2192 CTCACCATCCTTATCTGGCACTGGCCTTTCCACCAACCGGCCGCCAGAGCTACCTGGTGAC 2251
 |||
 Sbjct 5281 CTCACCATCCTTATCTGGCACTGGCCTTTCCACCAACCGGCCGCCAGAGCTACCTGGTGAC 5340



Score = 116 bits (60), Expect = 9e-22
 Identities = 60/60 (100%), Gaps = 0/60 (0%)
 Strand=Plus/Plus

Query 2252 ACCTGCACCTCGCTATGGCATGGCCAGCTGCCGCTCTGAGTGCTAACCGGAGCCTGCTAGCC 2311
 |||
 Sbjct 5401 ACCTGCACCTCGCTATGGCATGGCCAGCTGCCGCTCTGAGTGCTAACCGGAGCCTGCTAGCC 5460



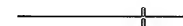
Score = 116 bits (60), Expect = 9e-22
 Identities = 60/60 (100%), Gaps = 0/60 (0%)
 Strand=Plus/Plus

Query 2312 AGTGCTGATGCTGTGGTCTTCCACCAACCGTGAGCTGCAAAACCGGCAATCTCTCTACCC 2371
 |||
 Sbjct 5521 AGTGCTGATGCTGTGGTCTTCCACCAACCGTGAGCTGCAAAACCGGCAATCTCTCTACCC 5580



Score = 116 bits (60), Expect = 9e-22
 Identities = 60/60 (100%), Gaps = 0/60 (0%)
 Strand=Plus/Plus

Query 2372 CTGGACCAAGAGCCACACGGACAGCCTTGGGCTCTGGGCTCCATGGAATCGCCAGTAAT 2431
 |||
 Sbjct 5641 CTGGACCAAGAGCCACACGGACAGCCTTGGGCTCTGGGCTCCATGGAATCGCCAGTAAT 5700



Score = 116 bits (60), Expect = 9e-22
 Identities = 60/60 (100%), Gaps = 0/60 (0%)
 Strand=Plus/Plus

Query 2492 TCAGATATCTTTGTACCTACGGTCGCTTGGAGCCTCTCTCTGGGCCACATCCCCACTA 2551
 |||
 Sbjct 5881 TCAGATATCTTTGTACCTACGGTCGCTTGGAGCCTCTCTCTGGGCCACATCCCCACTA 5940



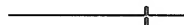
Score = 116 bits (60), Expect = 9e-22
 Identities = 60/60 (100%), Gaps = 0/60 (0%)
 Strand=Plus/Plus

Query 2612 GCAAAGCTGTACCGGCAGCTGGCCCCCTCATCTGCAGGTGGATGTGTTCCGGTCGCCCCAGC 2671
 |||
 Sbjct 6121 GCAAAGCTGTACCGGCAGCTGGCCCCCTCATCTGCAGGTGGATGTGTTCCGGTCGCCCCAGC 6180



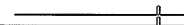
Score = 116 bits (60), Expect = 9e-22
 Identities = 60/60 (100%), Gaps = 0/60 (0%)
 Strand=Plus/Plus

Query 2672 GGACGGCCCCCTATGCGCTAAATTGTCTGCTGCCCACTTTGGCCCCGTACCGCTTCTACCTG 2731
 |||
 Sbjct 6241 GGACGGCCCCCTATGCGCTAAATTGTCTGCTGCCCACTTTGGCCCCGTACCGCTTCTACCTG 6300



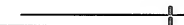
Score = 116 bits (60), Expect = 9e-22
 Identities = 60/60 (100%), Gaps = 0/60 (0%)
 Strand=Plus/Plus

Query 2732 GCCTTTGAGAACTCAGCATCGGGACTACATCACTGAGAAGTTCTGGCGCAATGCCCTG 2791
 |||
 Sbjct 6361 GCCTTTGAGAACTCAGCATCGGGACTACATCACTGAGAAGTTCTGGCGCAATGCCCTG 6420



Score = 116 bits (60), Expect = 9e-22
 Identities = 60/60 (100%), Gaps = 0/60 (0%)
 Strand=Plus/Plus

Query 2852 CCACCAGATGCCCTTTGTACACGTGGACGACTTCAGCTCTGCCCGTGAATGGCTGTCTTC 2911
 |||
 Sbjct 6601 CCACCAGATGCCCTTTGTACACGTGGACGACTTCAGCTCTGCCCGTGAATGGCTGTCTTC 6660



Score = 116 bits (60), Expect = 9e-22
 Identities = 60/60 (100%), Gaps = 0/60 (0%)
 Strand=Plus/Plus

Query 2972 GTGCGGCTCCTGGGTGACTGGAGGGAGCGCTTCTGCACCATCTGTGCCCGCTACCCCTTAC 3031
 |||
 Sbjct 6841 GTGCGGCTCCTGGGTGACTGGAGGGAGCGCTTCTGCACCATCTGTGCCCGCTACCCCTTAC 6900



Score = 116 bits (60), Expect = 9e-22
 Identities = 60/60 (100%), Gaps = 0/60 (0%)
 Strand=Plus/Plus

Query 3032 TTGCCCCGAGCCAGGCTCTATGAAGACCTTGAAGAGCTGTTCCAGGCTTGAACCTCCTGCT 3091
 |||
 Sbjct 6961 TTGCCCCGAGCCAGGCTCTATGAAGACCTTGAAGAGCTGTTCCAGGCTTGAACCTCCTGCT 7020



Score = 116 bits (60), Expect = 9e-22
 Identities = 60/60 (100%), Gaps = 0/60 (0%)
 Strand=Plus/Plus

Query 3152 CTTTGGTTCACCATGSCACTACCCCAAGGCTTTTCCTGTTTCAGTGAGCAGGAATTCAGGA 3211
 |||
 Sbjct 7201 CTTTGGTTCACCATGSCACTACCCCAAGGCTTTTCCTGTTTCAGTGAGCAGGAATTCAGGA 7260



Score = 116 bits (60), Expect = 9e-22
 Identities = 60/60 (100%), Gaps = 0/60 (0%)
 Strand=Plus/Plus

Query 3272 GAGACAATGAATTAATGAGGAGCATATGGGGAAGGTGGCTGAGGCTCCTGACTTACCTT 3331
 |||
 Sbjct 7441 GAGACAATGAATTAATGAGGAGCATATGGGGAAGGTGGCTGAGGCTCCTGACTTACCTT 7500



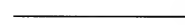
Score = 116 bits (60), Expect = 9e-22
 Identities = 60/60 (100%), Gaps = 0/60 (0%)
 Strand=Plus/Plus

Query 3332 GACCCATGGCTGAAGGCTCCATGCCCCATGGCTGGAGCTGGGACCCCTACACTTCTATAGTC 3391
 |||
 Sbjct 7561 GACCCATGGCTGAAGGCTCCATGCCCCATGGCTGGAGCTGGGACCCCTACACTTCTATAGTC 7620



Score = 116 bits (60), Expect = 9e-22
 Identities = 60/60 (100%), Gaps = 0/60 (0%)
 Strand=Plus/Plus

Query 3392 AAGGTGCTTAGCCTCAAGGTTGAGATGCACCTCTAGTACTCTGGGTGCAGACTGTACA 3451
 |||
 Sbjct 7681 AAGGTGCTTAGCCTCAAGGTTGAGATGCACCTCTAGTACTCTGGGTGCAGACTGTACA 7740



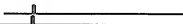
Score = 116 bits (60), Expect = 9e-22
 Identities = 60/60 (100%), Gaps = 0/60 (0%)
 Strand=Plus/Plus

Query 3452 CTGGGCGCAGGGGGTTGTGGAGGACAGTCAGATGATTCTGGGCTTTTGACACCAAGT 3511
 |||||||
 Sbjct 7801 CTGGGCGCAGGGGGTTGTGGAGGACAGTCAGATGATTCTGGGCTTTTGACACCAAGT 7860



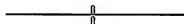
Score = 116 bits (60), Expect = 9e-22
 Identities = 60/60 (100%), Gaps = 0/60 (0%)
 Strand=Plus/Plus

Query 3512 TCCCCCAGGGAAAGAGGCACTACTAATAAAAACTGACAGAAATCTCTGGTCAAGTCT 3571
 |||||||
 Sbjct 7921 TCCCCCAGGGAAAGAGGCACTACTAATAAAAACTGACAGAAATCTCTGGTCAAGTCT 7980



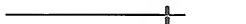
Score = 110 bits (57), Expect = 5e-20
 Identities = 59/60 (98%), Gaps = 0/60 (0%)
 Strand=Plus/Plus

Query 572 TGACATAGGGTCGGGTCGGGCGAGCGGAAGTGTAGGAGGTGATCCCCAAGGGATGCTGG 631
 |||||||
 Sbjct 2041 TGACATAGGGTCGGGTCGGGCGAGCGGAAGTGTAGGAGGTGATCCCCAAGGGATGCTGG 2100



Score = 110 bits (57), Expect = 5e-20
 Identities = 59/60 (98%), Gaps = 0/60 (0%)
 Strand=Plus/Plus

Query 1712 TCTTTGAGCAGAAGACGGGGTGGGTGGGGTAGGATTGGATAGTGGTATGCCAAGATT 1771
 |||||||
 Sbjct 4321 TCTTTGAGCAGAAGACGGGGTGGGTGGGGTAGGATTGGATAGTGGTATGCCAAGATT 4380



Score = 104 bits (54), Expect = 3e-18
 Identities = 58/60 (96%), Gaps = 0/60 (0%)
 Strand=Plus/Plus

Query 3212 TATAAGGAGAAGACTGGGCTGAGATACCTGGTGGGCTTTAGAGTAGGGGCCAGGATAA 3271
 |||||||
 Sbjct 7321 TATAAGGAGAAAAGCTGGGCTGAGATGCCCTGGTGGGCTTTAGAGTAGGGGCCAGGATAA 7380



Score = 62.2 bits (32), Expect = 1e-05
Identities = 32/32 (100%), Gaps = 0/32 (0%)
Strand=Plus/Plus

Query 1 ACAAACAGGAAGGACAGCAGGCTCTGGCAGCC 32
|||||
Sbjct 870 ACAAACAGGAAGGACAGCAGGCTCTGGCAGCC 901



Score = 52.6 bits (27), Expect = 0.011
Identities = 29/30 (96%), Gaps = 0/30 (0%)
Strand=Plus/Minus

Query 1585 CTCCTGCTCTGCTCTTCCTTCCTTCCTCTC 1614
|||||
Sbjct 4172 CTCCTGCTCTGCTCTTCCTTCCTTCCTCTC 4143



Score = 43.0 bits (22), Expect = 9.0
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Minus

Query 1601 TCCTTCCTTCCTTCCTTCCTTCCT 1622
|||||
Sbjct 4171 TCCTTCCTTCCTTCCTTCCTTCCT 4150

CPU time: 0.24 user secs. 0.03 sys. secs 0.27 total secs.